**RAW SEQUENCE LISTING**
PATENT APPLICATION *US/09/232,522*



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**This Raw Listing contains the General Information Section and up to the first 5 pages.**



SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Gately, Maurice K.
Presky, David H.

(ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Hoffmann-La Roche Inc.
(B) STREET: 340 Kingsland Street
(C) CITY: Nutley
(D) STATE: New Jersey
(E) COUNTRY: United States
(F) ZIP: 07110-1199

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Buchholz, Briana C.
(B) REGISTRATION NUMBER: 39,123
(C) REFERENCE/DOCKET NUMBER: CD 1048P

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 973-235-6208
(B) TELEFAX: 973-235-2363

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: mouse
(G) CELL TYPE: Hybridoma
(H) CELL LINE: HIL-12F3-16G2

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC        48
Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
 1               5                  10                  15

CTC ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC        96
Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn
            20                  25                  30

TGG ATC CGG AAA TTC CCA GGG AAT AAA TTT GAG TAC ATG GGA TTC ATA       144
Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile
        35                  40                  45

AGT TAT AGT GGT AGC ACT TAC AAT AAT CCA TCT CTC AAA AAT CGA GTC       192
Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
    50                  55                  60

TCC ATC ACT CGA GAC ACA TCC AAT AAC CAG TAC TAC CTG CAG TTG AGT       240
Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser
65                  70                  75                  80

TCT GTG ACT ACT GAG GAC TCA GCC ACA TAT TAC TGT GCA AGA TCT TCG       288
Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser
                85                  90                  95

GAT GCT TTG GAC TAC TGG GGC GCA GGG ACC ACG                           321
Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
 1               5                  10                  15

Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn
            20                  25                  30

Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile
        35                  40                  45

Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
    50                  55                  60

Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser
65                  70                  75                  80

Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser
                85                  90                  95

Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: mouse
(G) CELL TYPE: Hybridoma
(H) CELL LINE: HIL-12F3-20E11

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..306

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153       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
154
155   GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC         48
156   Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu
157     1               5                  10                  15
158
159   ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG         96
160   Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp
161                 20                  25                  30
162
163   ATC CGG AAA TTC CCA GAT AAT ACA CTT GAG TAC ATG GGA TAC ATA AGT        144
164   Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser
165             35                  40                  45
166
167   TAC AGT GGT AGT ACT TAC TAC AAT CCA TCT CTC AGA AGT CGA ATC TCC        192
168   Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser
169         50                  55                  60
170
171   ATC ACT CGA GAC ACA TCC AAG AAC CAG TAC TCC ATG CAG TTG AAT TCT        240
172   Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser
173    65                  70                  75                  80
174
175   GTG ACT ACT GAG GAC ACA GCC ACA TAT TAC TGT GCA AGA TCC TCG GAT        288
176   Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp
177                   85                  90                  95
178
179   GCT ATG GAC TAC TGG GGC GC                                            308
180   Ala Met Asp Tyr Trp Gly
181               100
182
183
184   (2) INFORMATION FOR SEQ ID NO:4:
185
186         (i) SEQUENCE CHARACTERISTICS:
187               (A) LENGTH: 102 amino acids
188               (B) TYPE: amino acid
189               (D) TOPOLOGY: linear
190
191       (ii) MOLECULE TYPE: protein
192
193       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
194
195   Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu
196     1               5                  10                  15
197
198   Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp
199                 20                  25                  30
200
201   Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser
202             35                  40                  45
203
204   Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser
205         50                  55                  60
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```
206
207   Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser
208    65                  70                  75                  80
209
210   Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp
211                    85                  90                  95
212
213   Ala Met Asp Tyr Trp Gly
214                100
215
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**SEQUENCE VERIFICATION REPORT**
PATENT APPLICATION *US/09/232,522*

DATE: 01/29/1999
TIME: 11:17:21

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